

SEQUENCE LISTING

<110> HONJO, TASUKU
KATO, KEIZO
TADA, HIDEAKI

<120> POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM

<130> Q58771

<140> 09/529,064

<141> 2000-04-07

<150> PCT/JP98/04515

<151> 1998-10-06

<150> HEI-9-274673

<151> 1997-10-07

<160> 28

<170> PatentIn Ver. 2.1

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<211> 160

<212> PRT

<213> Mus musculus

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1 5 10 15

Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
20 25 30

Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
35 40 45

Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
50 55 60

Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
65 70 75 80

Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
85 90 95

Val Asn Thr Ser Ile Pro Phe Ser Phe Glu Gly Ile Leu Phe Pro Lys
100 105 110

Gly His Tyr Arg Cys Val Ala Glu Ala Ile Ala Gly Asp Thr Glu Glu
115 120 125

Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile His Arg Arg Asp Val Asn
130 135 140

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 ttcgagggaa tactatttcc taagggccat tacagatgtg ttgcagaagc tattgtctggg 420
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 -5 -1 1 5 10

tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
 Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
 15 20 25

cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
 Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
 30 35 40

gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
 Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
 45 50 55

tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt 292
 Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
 60 65 70

aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga 340
 Lys Glu Val Leu Cys His Gly His Asp Asp Tyr Ser Phe Cys Arg
 75 80 85 90

gct ctg aaa gga gag act gtg aat aca tca ata cca ttc tct ttc gag 388
 Ala Leu Lys Gly Glu Thr Val Asn Thr Ser Ile Pro Phe Ser Phe Glu
 95 100 105

gga ata cta ttt cct aag ggc cat tac aga tgt gtt gca gaa gct att 436
 Gly Ile Leu Phe Pro Lys Gly His Tyr Arg Cys Val Ala Glu Ala Ile
 110 115 120

gct ggg gat act gaa gaa aag ctc ttc tgt ttg aat ttc acc atc att 484
 Ala Gly Asp Thr Glu Glu Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile
 125 130 135

cac cgc cgt gat gtc aat tagaatatgc tgaatacaca cacacacaca 532
 His Arg Arg Asp Val Asn
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 <212> PRT
 <213> Mus musculus

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 1 5 10 15
 Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
 20 25 30
 Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
 35 40 45
 Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
 50 55 60
 Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
 65 70 75 80
 Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Gly Tyr
 85 90 95
 Ala Ile

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 aaattcccta ttccaattag ttctgaaccc tgcataagac tgaggggaac caatggattt 180
 gtgatgttg agttcattcc aagaggaaac ttaaaattatt tatatttcaa cctattcacc 240
 agtgtcaact ccatagagtt gccgaagcgt aaggaagtgc tgtgccatgg acatgatgat 300
 gactattctt ttgacagagc tctgaaagga ggatatgcta tt 342

<210> 6
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 Leu Ser Pro Ile Leu Thr Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn
 -5 -1 1 5 10

tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
 Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
 15 20 25

cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
 Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
 30 35 40

gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
 Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
 45 50 55

tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt 292
 Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
 60 65 70

aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga 340
 Lys Glu Val Leu Cys His Gly His Asp Asp Asp Tyr Ser Phe Cys Arg
 75 80 85 90

gct ctg aaa gga gga tat gct att tagaaaaat gagactgtga ataatcaat 394
 Ala Leu Lys Gly Gly Tyr Ala Ile
 95

accattctct ttgaggggaa tactatttcc taagggccat tacagatgtg ttgcagaagc 454
 tattgctggg gatactgaag aaaagctctt ctgtttgaat ttcacctca ttcaccgccg 514
 tgaagtcaat tagaatatgc tgaatacaca cacacacaca cacacacaca cacacatatg 574
 tatatatata tttttttacc ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 630

<210> 7

<211> 160

<212> PRT

<213> Homo sapiens

<400> 7

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
 -15 -10 -5 -1

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
 1 5 10 15

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
 20 25 30

Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys Gly Leu Leu His Ile Phe
 35 40 45

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
 50 55 60

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
 65 70 75 80

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
 85 90 95

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
 100 105 110

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
 115 120 125

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
 130 135 140

<210> 8

<211> 480

<212> DNA

<213> Homo sapiens

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caatacccaa tttcaattaa tgttaacccc tgtatagaat tgaaggagatc caaaggatta 180
ttgcacattt tctacattcc aaggagagat ttaagcaat tatatttcaa tctctatata 240
actgtcaaca ccatgaatct tccaaagcgc aaagaagtta tttgccgagg atctgatgac 300
gattactctt tttgcagagc tctgaaggga gagactgtga atacaacaat atcattctcc 360
ttcaagggaa taaaattttc taagggaaaa tacaaatgtg ttggttgagg tatttctggg 420
agcccagaag aaatgctctt ttgcttgagg tttgtcatcc tacaccaacc taatttcaaa 480

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Phe Ser Ser Ile Phe Thr Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn
-5 -1 1 5 10

tca tcc gat gca agt att tca tac acc tac tgt gat aaa atg caa tac 147
Ser Ser Asp Ala Ser Ile Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr
15 20 25

cca att tca att aat gtt aac ccc tgt ata gaa ttg aaa gga tcc aaa 195
Pro Ile Ser Ile Asn Val Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys
30 35 40

gga tta ttg cac att ttc tac att cca agg aga gat tta aag caa tta 243
Gly Leu Leu His Ile Phe Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu
45 50 55

tat ttc aat ctc tat ata act gtc aac acc atg aat ctt cca aag cgc 291
Tyr Phe Asn Leu Tyr Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg
60 65 70

aaa gaa gtt att tgc cga gga tct gat gac gat tac tct ttt tgc aga 339
Lys Glu Val Ile Cys Arg Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg
75 80 85 90

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gct ctg aag gga gag act gtg aat aca ata tca ttc tcc ttc aag 387
 Ala Leu Lys Gly Glu Thr Val Asn Thr Thr Ile Ser Phe Ser Phe Lys
 95 100 105

gga ata aaa ttt tct aag gga aaa tac aaa tgt gtt gtt gaa gct att 435
 Gly Ile Lys Phe Ser Lys Gly Lys Tyr Lys Cys Val Val Glu Ala Ile
 110 115 120

tct ggg agc cca gaa gaa atg ctc ttt tgc ttg gag ttt gtc atc cta 483
 Ser Gly Ser Pro Glu Glu Met Leu Phe Cys Leu Glu Phe Val Ile Leu
 125 130 135

cac caa cct aat tca aat tagaataaat tgagtattta aaaaaaaaaa aaaaaaaaa 539
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<210> 10

<211> 162

<212> PRT

<213> Mus musculus

<400> 10

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 -15 -10 -5

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 -1 1 5 10

Cys Asn Ser Gly Gly Leu Glu Val Val Tyr Gln Ser Cys Asp Pro Leu
 15 20 25

Gln Asp Phe Gly Leu Ser Ile Asp Gln Cys Ser Lys Gln Ile Gln Ser
 30 35 40 45

Asn Leu Asn Ile Arg Phe Gly Ile Ile Leu Arg Gln Asp Ile Arg Lys
 50 55 60

Leu Phe Leu Asp Ile Thr Leu Met Ala Lys Gly Ser Ser Ile Leu Asn
 65 70 75

Tyr Ser Tyr Pro Leu Cys Glu Glu Asp Gln Pro Lys Phe Ser Phe Cys
 80 85 90

Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly Pro Val Asn Asn
 95 100 105

Pro Gly Leu Asp Val Pro Gln Gly Glu Tyr Gln Leu Leu Leu Glu Leu
 110 115 120 125

Tyr Asn Glu Asn Arg Ala Thr Val Ala Cys Ala Asn Ala Thr Val Thr
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Ser Ser

<210> 11

<211> 486

<212> DNA

<213> Mus musculus

<400> 11

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gtctaccaga gctgtgatcc cttacaggat tttggccttt ccattgacca gtgttccaag 180
cagatccaat caaatctcaa cattagattt ggcatcattc tgagacagga taccagaaag 240
ctgtttctgg acataactct gatggcaaaa ggctcttcta tcttgaacta ctcctatccc 300
ctttgtgagg aggaccagcc caagtctcta ttctgtggaa gaagaaaagg agaacagata 360
tactatgccg gccctgtcaa taacctggga cttgatgttc cacaggggga atatcagctc 420
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<211> 996

<212> DNA

<213> Mus musculus

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<222> (91)..(147)

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ttaccattgg gcacacacaa cccctcgcgc atg aat ggt gtc gca gct gcc ctc 114

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Met Asn Gly Val Ala Ala Leu

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-15

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ctt gtg tgg att ctg act tct ccg agc agc agt gac cat ggc agc gaa 162

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Leu Val Trp Ile Leu Thr Ser Pro Ser Ser Asp His Gly Ser Glu

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-10

-5

-1

1

5

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aat ggt tgg ccc aag cac acg gcc tgc aac agt ggg ggc ttg gaa gta 210

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Asn Gly Trp Pro Lys His Thr Ala Cys Asn Ser Gly Gly Leu Glu Val

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10

15

20

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gtc tac cag agc tgt gat ccc tta cag gat ttt ggc ctt tcc att gac 258

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Val Tyr Gln Ser Cys Asp Pro Leu Gln Asp Phe Gly Leu Ser Ile Asp

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25

30

35

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cag tgt tcc aag cag atc caa tca aat ctc aac att aga ttt ggc atc 306

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Gln Cys Ser Lys Gln Ile Gln Ser Asn Leu Asn Ile Arg Phe Gly Ile

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40

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50

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att ctg aga cag gat atc aga aag ctg ttt ctg gac ata act ctg atg 354

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Ile Leu Arg Gln Asp Ile Arg Lys Leu Phe Leu Asp Ile Thr Leu Met

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55

60

65


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gca aaa ggc tct tct att ctg aac tac tcc tat ccc ctt tgt gag gag 402
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70 75 80 85

gac cag ccc aag ttc tca ttc tgt gga aga aga aaa gga gaa cag ata 450
Asp Gln Pro Lys Phe Ser Phe Cys Gly Arg Arg Lys Gly Glu Gln Ile
90 95 100

tac tat gcc ggc cct gtc aat aac cct gga ctt gat gtt cca cag gga 498
Tyr Tyr Ala Gly Pro Val Asn Asn Pro Gly Leu Asp Val Pro Gln Gly
105 110 115

gaa tat cag ctc ttg ctg gaa ctg tac aat gaa aac cgt gct act gtg 546
Glu Tyr Gln Leu Leu Leu Glu Tyr Asn Glu Asn Arg Ala Thr Val
120 125 130

gct tgt gcc aat gcc act gtc acc tcc tcc tgagcatgggt ctgcaaggaa 596
Ala Cys Ala Asn Ala Thr Val Thr Ser Ser
135 140

atgcacagta aactcaatct caggggaccc caaggtccct ggactcacct agctgcaaga 656

accactgata accaagagag gctttacaaa gaaatttctt gtgggtcact cttccgatct 716

tagctccagg gacagatggt cccagaccca acagatgtaa taaccctca aaaactatct 776

atttctgagg accctgagta gtcttgaagc cctattgtag tacctctcct tatgtaatta 836

cgtttcacaa aagctacttc cttgctgct ccttagcaac acttccttga agttgcctgg 896

gatgtaaaaa ataaaataaa ataaaataaa ataaaataaa ataaaataaa atgaaatgaa 956

aaataaataa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 996

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<211> 162
<212> PRT
<213> Homo sapiens

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-1 1 5 10

Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln Ser Cys Asp Pro Leu
15 20 25

Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser Lys Gln Leu Lys Ser
30 35 40

Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg Glu Asp Ile Lys Glu
45 50 55 60

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Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly Ser Ser Val Leu Asn
65 75

Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro Lys Phe Ser Phe Cys
80 85 90

Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly Pro Val Asn Asn
95 100 105

Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln Val Leu Leu Glu Leu
110 115 120

Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala Asn Ala Thr Ile Met
125 130 135 140

Cys Ser

<210> 14

<211> 486

<212> DNA

<213> Homo sapiens

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ctctaccaga gttgcgattc attacaagat tttggctttt ctgttgaaaa gtgttccaag 180
caattaaaaat caaatatcaa cattagattt ggaattattc tgagagagga catcaaagag 240
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atctgtgagg cggctctgcc caagttttct ttctgtggaa gaaggaaaag agagcagatt 360
tactatgctg ggctctgcaa taatctgtaa tttactatto ctcagggaga ataccaggtt 420
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tgctcc 486

<210> 15

<211> 877

<212> DNA

<213> Homo sapiens

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<222> (76)..(501)

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<221> CDS

<222> (16)..(501)

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-20 -15 -10

ctg att ttt ccc agc tgc agt gga ggc ggc ggt ggg aaa gcc tgg ccc 99
 Leu Ile Phe Pro Ser Cys Ser Gly Gly Gly Gly Lys Ala Trp Pro
 -5 -1 1 5

aca cac gtg gtc tgt agc gac agc ggc ttg gaa gtg ctc tac cag agt 147
 Thr His Val Val Cys Ser Asp Ser Gly Leu Glu Val Leu Tyr Gln Ser
 10 15 20

tgc gat cca tta caa gat ttt ggc ttt tct gtt gaa aag tgt tcc aag 195
 Cys Asp Pro Leu Gln Asp Phe Gly Phe Ser Val Glu Lys Cys Ser Lys
 25 30 35 40

caa tta aaa tca aat atc aac att aga ttt gga att att ctg aga gag 243
 Gln Leu Lys Ser Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg Glu
 45 50 55

gac atc aaa gag ctt ttt ctt gac cta gct ctc atg tct caa ggc tca 291
 Asp Ile Lys Glu Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly Ser
 60 65 70

tct gtt ttg aat ttc tcc tat ccc atc tgt gag gcg gct ctg ccc aag 339
 Ser Val Leu Asn Phe Ser Tyr Pro Ile Cys Glu Ala Leu Pro Lys
 75 80 85

ttt tct ttc tgt gga aga agg aaa gga gag cag att tac tat gct ggg 387
 Phe Ser Phe Cys Gly Arg Lys Gly Glu Gln Ile Tyr Tyr Ala Gly
 90 95 100

cct gtc aat aat cct gaa ttt act att cct cag gga gaa tac cag gtt 435
 Pro Val Asn Asn Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln Val
 105 110 115 120

ttg ctg gaa ctg tac act gaa aaa cgg tcc acc gtg gcc tgt gcc aat 483
 Leu Leu Glu Leu Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala Asn
 125 130 135

gct act atc atg tgc tcc tgactgtggc ctgtagcaaa aatcacagcc 531
 Ala Thr Ile Met Cys Ser
 140

agctgcactc cgtgggaacct ccaagctcct ctgactgaac ctactgtggg aggagaagca 591

gctgatgaca gagagaggct ctacaaagaa gcgcccccaa agagtgcagc tgctaatttt 651

agtccccagga ccagacatcc ccagactcca cagatgtaat gaagtcccg aatgtatctg 711

tttctaagga gcctcttggc agtccttaag cagtcttgag ggtoaatcct ttttctctaa 771

ttggtgcgct ccaccagac tcacctgctt ttcaactttt taggagtgtc tctcacagt 831

taccaagaat aaagaaagct ggccacccaaa aaaaaaaaaa aaaaaa 877

<210> 16

<211> 40

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: SalI-random
      9mer to synthesize a single strand cDNA

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<221> modified_base
<222> (32...40)
<223> "n" represents a, t, c, or g

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gagacggtaa tacgacgcac agtaggtcga cnnnnnnnnn      40

<210> 17
<211> 23
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EcoRI adapter

<400> 17
ccgcgaattc tgactaactg att      23

<210> 18
<211> 25
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: EcoRI adapter

<400> 18
aatcagttag tcagaattcg cggac      25

<210> 19
<211> 23
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Forward primer

<400> 19
ccgcgaattc tgactaactg att      23

<210> 20
<211> 24
<212> DNA
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<220>
<223> Description of Unknown Organism: Reverse primer

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<400> 20
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<210> 21
 <211> 34
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: 3' Race adapter primer

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<210> 22
 <211> 27
 <212> DNA
 <213> Mus musculus

<220>
 <223> OHP106F2 primer

<400> 22
 ctcccatatt gactgaatct gagaagc 27

<210> 23
 <211> 17
 <212> DNA
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<220>
 <223> Description of Unknown Organism: Universal Amplification primer

<400> 23
 ggccacgcgt cgactac 17

<210> 24
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 <213> Mus musculus

<220>
 <223> OHP106F1 primer

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<210> 25
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 Amplification primer

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 <211> 30
 <212> DNA
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<220>
 <223> XbaI-mouse OHP106F primer

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<220>
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